

FIGURE 1A

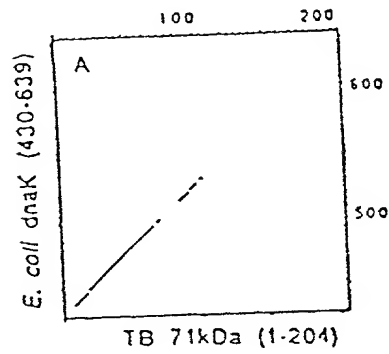
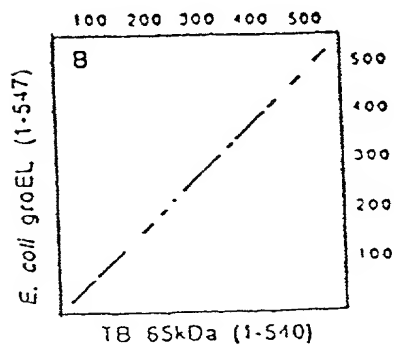


FIGURE 1B



	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWGS							
GROEL	-----MA-----AKDVKFGNDARVKMLRGVNVVLADAVKVTLGPKGRNVVLDKSFGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEZAGDGTATTATVLARSIKEGFEKISKGANPVEI							
GROEL	PTITKDGVSVAEIEFEDKXFENMGAQMVKEVASKANDAAGDGTATTATVLAQAIITEGLKAVAAGMNPMDL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
GROEL	KRGIDKAVTAAVEELKALSVPSCSDSKAIAQVGTISANSDETGVKLIAMDKVGKEGVITVEDGTGLQDE							
	211	220	230	240	250	260	270	280
HUMP1	LEIIIEGMKFDRGYISPYFINTSKGQKCEFDQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVITAEVDVG							
GROEL	LDVVEGMQFDRGYLSPYFINKPETGAVELESFFILLADKKISNIREMLPVLEAVAKAGKPLLIITAEVDEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV							
GROEL	EALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKKGKGDKAQIEKRIQEIIEQLDVTTSSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDP							
GROEL	NKDTTTIIDGVGEEAAIQGRVAQIROQIEEATSDYDREKLQERVAKLGGVAVIKVGAATEVEMKEKKAF							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIRKTLKIPAMTIKAGVEGSL							
GROEL	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEQNVVSSSL-RAMEAPLRQIVLNCGEFSPV							
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGGMG							
GROEL	ANTVKGGDGNYGYNAAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKND-AADLG							
	561	570						
HUMP1	MGGMGG--GMGGGMF							
GROEL	AGGMGGMGGMGGMM-							

Total score = 4667, 5 breaks
 276 identities out of 545 possible matches between residues

25 random runs
 Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

FIGURE 3

	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWGS							
ML65K	M-----AKTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNVVLEKKWGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVLRSLIAKEGFEKISKGANPVEI							
ML65K	PTITNDGVSLIAKEIELEDPEYKIGAEVLVKEVAKKTCDVAGDGTATVLAQALVKEGLRNVAAGANPLGL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
ML65K	KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVIIVVEESNTFGLQ							
	211	220	230	240	250	260	270	280
HUMP1	LEIIIEGMKFDKRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANAHKPLVIAEDVDG							
ML65K	LELTEGMRFDKGYISGYFVTDARQEAVLEEPYILLVSSKVVSTVKDILLPLEKVIQAGKSLIIAEDVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNLRLKVGLQVAVKAPGFGDNRKNQLKDMATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV							
ML65K	EALSTLVVNKIRGTFSKAVKAPGFGDNRKAMLDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKKGKDKAQIEKRIQEIIEQLDVTTSYEYKEKLNERLAKLSGVAVLKVGGSDDVEVNEKKDR							
ML65K	TKDETTIVEGAGDTDAIAGRVAQIRTEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHR							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIRKTLKIPAMTIKNAAGVEGSLI							
ML65K	IEDAVRNAKAAVEEGIVAGGGVTLLQAAPALDKLKTGDEAT-GANIVKVALEAPLKQIAFNSGMEPGV							
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMG							
ML65K	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSAALQNAASIAGLFTT-EAVVADKPEKTAAPASD							
	561	570						
HUMP1	MGGMGGGGMGGGMF							
ML65K	TGGMGG-MD---F							

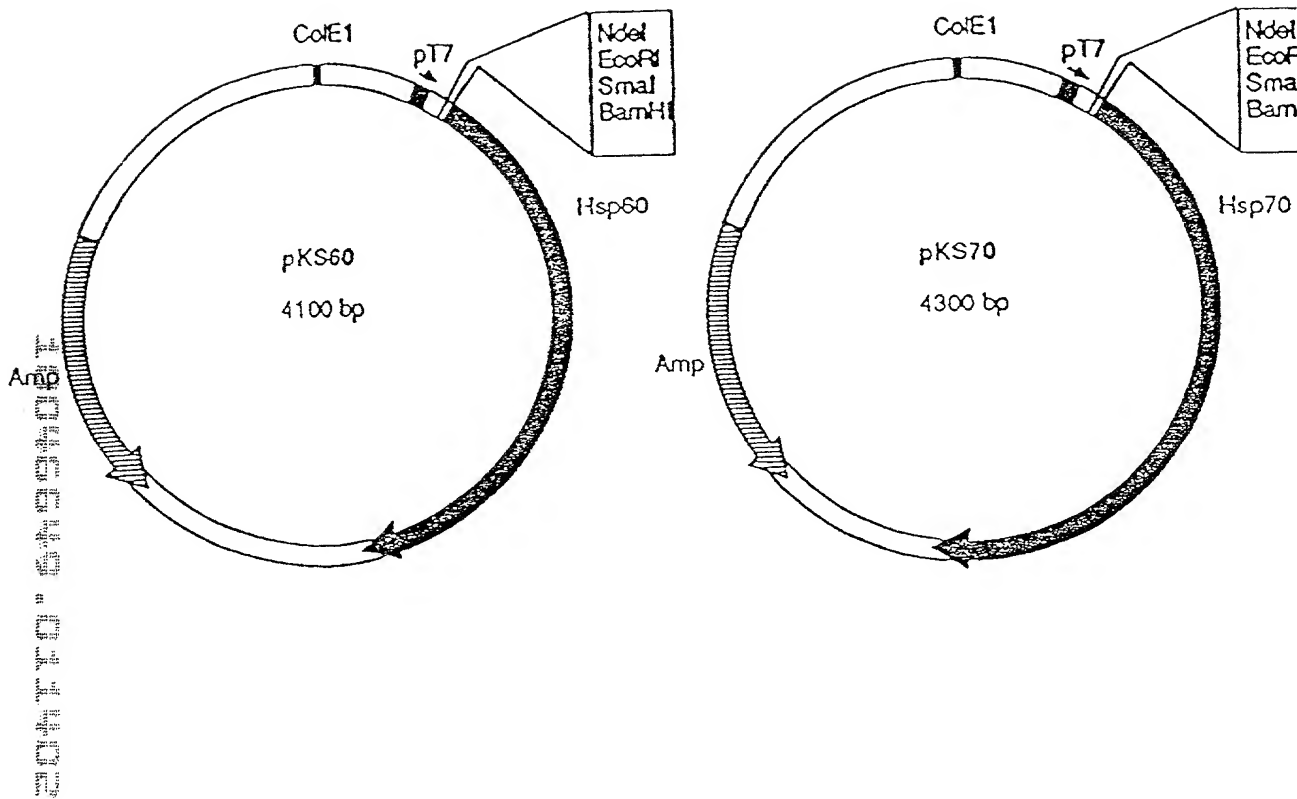
Total score = 4552, 7 breaks
 255 identities out of 540 possible matches between residues

25 random runs
 Alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.15

Inventors: Richard A. Young, *et al.*

Alignment score = 49.36 SD Standard deviation = 23.23 Mean = 3413.16

Figure 5



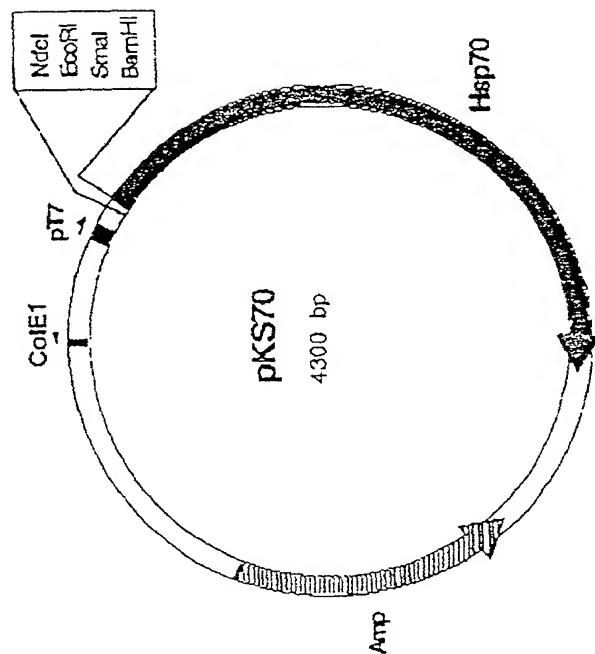
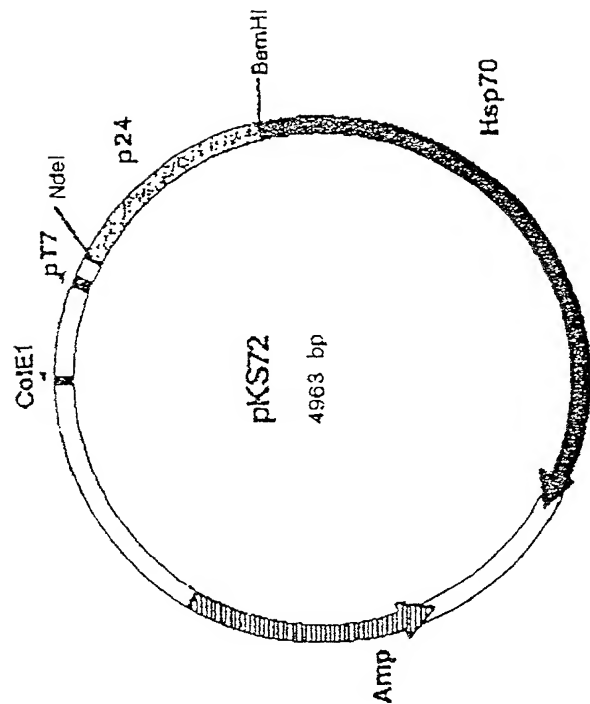


FIGURE 6

anti-p24 antibody titer
(3 weeks after boost)

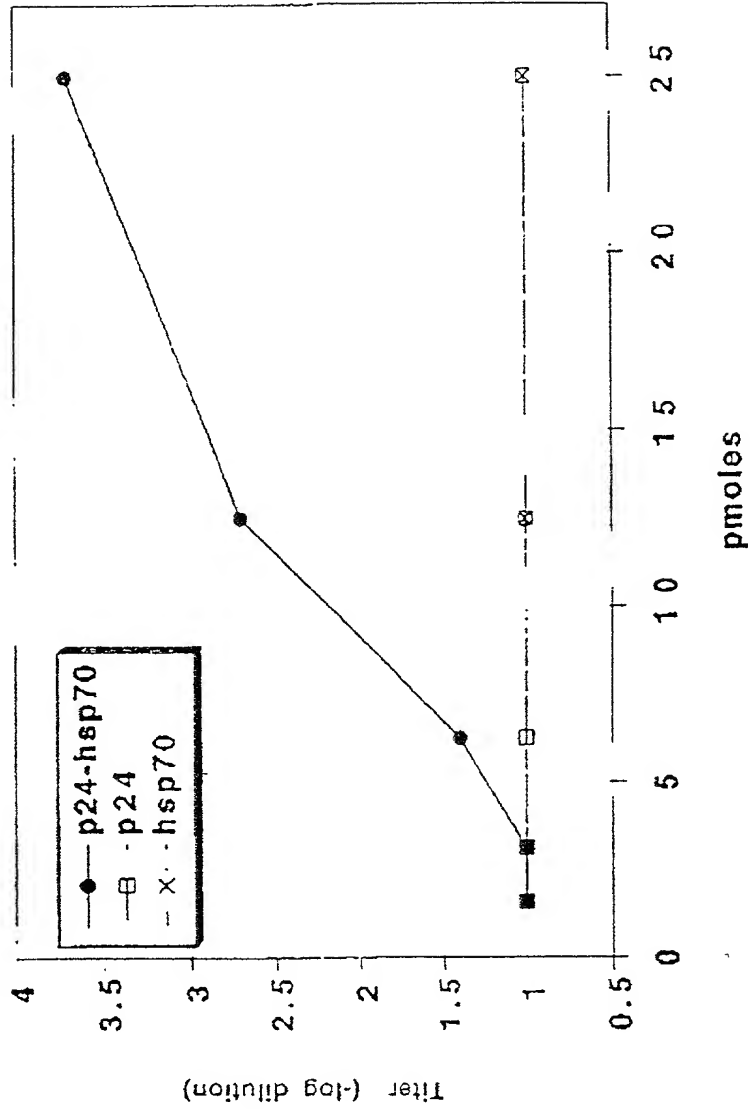


FIGURE 7